

Amendments to the Claims

Please amend the claims in the application as shown below in the list of claims.

List of Claims

1-20. Cancelled.

21. (Previously presented) A process for the production of an L-amino acid comprising:
- a) culturing a recombinant microorganism from the Enterobacteriaceae family in a fermentation medium, wherein;
 - i) said recombinant microorganism produces said L-amino acid;
 - ii) said recombinant microorganism has been transformed with a vector comprising an open reading frame (ORF) that encodes a protein comprising the amino acid sequence of SEQ ID NO:4;
 - iii) said ORF is overexpressed in said recombinant microorganism by increasing the copy number of said ORF or by linking said ORF to a promoter;
 - b) allowing said fermentation medium or said recombinant microorganism to become enriched in said L-amino acid; and
 - c) isolating said L-amino acid.
22. (Currently amended) The process of claim 21, wherein said ORF encodes a protein that consists of the amino acid sequence of SEQ ID NO:4.
23. (Previously presented) The process of claim 21 wherein some or all of the constituents of said fermentation medium and/or the biomass of said recombinant microorganism are isolated with said L-amino acid.
24. (Previously presented) The process of claim 21 wherein said ORF that encodes a protein with the amino acid sequence of SEQ ID NO:4 comprises the nucleotide sequence of SEQ ID NO:3.

25. (Previously presented) The process of claim 24 wherein said ORF that encodes a protein with the amino acid sequence of SEQ ID NO:4 consists of the nucleotide sequence of SEQ ID NO:3.
26. (Previously presented) The process of claim 21, wherein the genus of said recombinant microorganism is selected from the group consisting of: *Escherichia*; *Erwinia*; *Providencia*; and *Serratia*.
27. (Currently amended) The process of claim 21, wherein said microorganism overexpresses said ORF and, in addition, the activity of one or more additional *E. coli* genes is overexpressed, said one or more additional genes being selected from the group consisting of:
 - a) the *E. coli* thrABC operon coding for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase;
 - b) the *C. glutamicum* pyc gene coding for pyruvate carboxylase;
 - c) the *E. coli* pps gene for phosphoenolpyruvate synthase;
 - d) the *E. coli* ppc gene coding for phosphoenolpyruvate carboxylase;
 - e) the *E. coli* genes pntA and pntB coding for transhydrogenase;
 - f) the *E. coli* rhtB gene imparting homoserine resistance;
 - g) the *E. coli* mqo gene coding for malate:quinone oxidoreductase;
 - h) the *E. coli* rhtC gene imparting threonine resistance;
 - i) the *C. glutamicum* thrE gene coding for the threonine-export protein;
 - j) the *E. coli* gdhA gene coding for glutamate dehydrogenase;
 - k) the *E. coli* hns gene coding for the DNA binding protein HLP-II;
 - l) the *E. coli* pgm gene coding for phosphoglucomutase;
 - m) the *E. coli* fba gene coding for fructose biphosphate aldolase;
 - n) the *E. coli* ptsH gene coding for phosphohistidine protein hexose phosphotransferase;
 - o) the *E. coli* ptsI gene coding for enzyme I of the phosphotransferase system;
 - p) the *E. coli* crr gene coding for the glucose-specific IIA component;
 - q) the *E. coli* ptsG gene coding for the glucose-specific IIBC component;

- r) the *E. coli* lrp gene coding for the regulator of the leucine regulon;
- s) the *E. coli* csrA gene coding for the global regulator Csr;
- t) the *E. coli* fadR gene coding for the regulator of the fad regulon;
- u) the *E. coli* iclR gene coding for the regulator of central intermediary metabolism;
- v) the *E. coli* mopB gene coding for the 10 kDa chaperon;
- w) the *E. coli* ahpC gene coding for the small subunit of alkyl hydroperoxide reductase;
- x) the *E. coli* ahpF gene coding for the large subunit of alkyl hydroperoxide reductase;
- y) the *E. coli* cysK gene coding for cysteine synthase A;
- z) the *E. coli* cysB gene coding for the regulator of the cys regulon;
- aa) the *E. coli* cysJ gene coding for the flavoprotein of NADPH sulfite reductase;
- bb) the *E. coli* cysI gene coding for the haemoprotein of NADPH sulfite reductase;
- cc) the *E. coli* cysH gene coding for adenylyl sulfate reductase;
- dd) the *E. coli* phoB gene coding for the positive regulator PhoB of the pho regulon;
- ee) the *E. coli* phoR gene coding for the sensor protein of the pho regulon;
- ff) the *E. coli* phoE gene coding for protein E of the outer cell membrane;
- gg) the *E. coli* pykF gene coding for pyruvate kinase I, which is stimulated by fructose;
- hh) the *E. coli* pfkB gene coding for 6-phosphofructokinase II;
- ii) the *E. coli* malE gene coding for the periplasmic binding protein of maltose transport;
- jj) the *E. coli* sodA gene coding for superoxide dismutase;
- kk) the *E. coli* rseA gene coding for a membrane protein with anti-sigmaE activity;
- ll) the *E. coli* rseC gene coding for a global regulator of the sigmaE factor;
- mm) the *E. coli* sucA gene coding for the decarboxylase subunit of 2-ketoglutarate dehydrogenase;
- nn) the *E. coli* sucB gene coding for the dihydrolipoyl transsuccinase E2 subunit of 2-ketoglutarate dehydrogenase;

- oo) the *E. coli* sucC gene coding for the β -subunit of succinyl-CoA synthetase;
 - pp) the *E. coli* sucD gene coding for the α -subunit of succinyl-CoA synthetase;
 - qq) the *E. coli* adk gene coding for adenylate kinase;
 - rr) the *E. coli* hdeA gene coding for a periplasmic protein with chaperonin-type function;
 - ss) the *E. coli* hdeB gene coding for a periplasmic protein with chaperonin-type function;
 - tt) the *E. coli* icd gene coding for isocitrate dehydrogenase;
 - uu) the *E. coli* mglB gene coding for the periplasmic, galactose-binding transport protein;
 - vv) the *E. coli* lpd gene coding for dihydrolipoamide dehydrogenase;
 - ww) the *E. coli* aceE gene coding for the E1 component of the pyruvate-dehydrogenase complex;
 - xx) the *E. coli* aceF gene coding for the E2 component of the pyruvate-dehydrogenase complex;
 - yy) the *E. coli* pepB gene coding for aminopeptidase B;
 - zz) the *E. coli* aldH gene coding for aldehyde dehydrogenase,
 - aaa) the *E. coli* bfr gene coding for the iron-storage homoprotein;
 - bbb) the *E. coli* udp gene coding for uridine phosphorylase; and
 - ccc) the *E. coli* rseB gene coding for the regulator of sigmaE-factor activity.
28. (Previously presented) The process of claim 21, wherein said L-amino acid is selected from the group consisting of: L-threonine; L-lysine; L-isoleucine, L-valine, L-methionine, and L-homoserine.
29. (Previously presented) The process of claim 21, wherein said L-amino acid is either L-threonine or L-lysine.
30. (Currently amended) The process of claim 28, wherein said ORF encodes a protein that consists of the amino acid sequence of SEQ ID NO:4.

31. (Previously presented) The process of claim 28, wherein some or all of the constituents of said fermentation medium and/or the biomass of said recombinant microorganism are isolated with said L-amino acid.
32. (Previously presented) The process of claim 28, wherein said ORF that encodes a protein with the amino acid sequence of SEQ ID NO:4 comprises the nucleotide sequence of SEQ ID NO:3.
33. (Previously presented) The process of claim 32 wherein said ORF that encodes a protein with the amino acid sequence of SEQ ID NO:4 consists of the nucleotide sequence of SEQ ID NO:3.
34. (Previously presented) The process of claim 28, wherein the genus of said recombinant microorganism is selected from the group consisting of: *Escherichia*; *Erwinia*; *Providencia*; and *Serratia*.
35. (Currently amended) The process of claim 28, wherein said microorganism overexpresses said ORF and, in addition, the activity of one or more additional *E. coli* genes is overexpressed, said one or more additional genes being selected from the group consisting of:
 - a) the *E. coli* thrABC operon coding for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase;
 - b) the *C. glutamicum* pyc gene coding for pyruvate carboxylase;
 - c) the *E. coli* pps gene for phosphoenolpyruvate synthase;
 - d) the *E. coli* ppc gene coding for phosphoenolpyruvate carboxylase;
 - e) the *E. coli* genes pntA and pntB coding for transhydrogenase;
 - f) the *E. coli* rhtB gene imparting homoserine resistance;
 - g) the *E. coli* mqo gene coding for malate:quinone oxidoreductase;
 - h) the *E. coli* rhtC gene imparting threonine resistance;
 - i) the *C. glutamicum* thrE gene coding for the threonine-export protein;
 - j) the *E. coli* gdhA gene coding for glutamate dehydrogenase;

- k) the *E. coli* hns gene coding for the DNA binding protein HLP-II;
- l) the *E. coli* pgm gene coding for phosphoglucomutase;
- m) the *E. coli* fba gene coding for fructose biphosphate aldolase;
- n) the *E. coli* ptsH gene coding for phosphohistidine protein hexose phosphotransferase;
- o) the *E. coli* ptsI gene coding for enzyme I of the phosphotransferase system;
- p) the *E. coli* crr gene coding for the glucose-specific IIA component;
- q) the *E. coli* ptsG gene coding for the glucose-specific IIBC component;
- r) the *E. coli* lrp gene coding for the regulator of the leucine regulon;
- s) the *E. coli* csrA gene coding for the global regulator Csr;
- t) the *E. coli* fadR gene coding for the regulator of the fad regulon;
- u) the *E. coli* iclR gene coding for the regulator of central intermediary metabolism;
- v) the *E. coli* mopB gene coding for the 10 kDa chaperon;
- w) the *E. coli* ahpC gene coding for the small subunit of alkyl hydroperoxide reductase;
- x) the *E. coli* ahpF gene coding for the large subunit of alkyl hydroperoxide reductase;
- y) the *E. coli* cysK gene coding for cysteine synthase A;
- z) the *E. coli* cysB gene coding for the regulator of the cys regulon;
- aa) the *E. coli* cysJ gene coding for the flavoprotein of NADPH sulfite reductase;
- bb) the *E. coli* cysI gene coding for the haemoprotein of NADPH sulfite reductase;
- cc) the *E. coli* cysH gene coding for adenylyl sulfate reductase;
- dd) the *E. coli* phoB gene coding for the positive regulator PhoB of the pho regulon;
- ee) the *E. coli* phoR gene coding for the sensor protein of the pho regulon;
- ff) the *E. coli* phoE gene coding for protein E of the outer cell membrane;
- gg) the *E. coli* pykF gene coding for pyruvate kinase I, which is stimulated by fructose;
- hh) the *E. coli* pfkB gene coding for 6-phosphofructokinase II;

- ii) the *E. coli* malE gene coding for the periplasmic binding protein of maltose transport;
- jj) the *E. coli* sodA gene coding for superoxide dismutase;
- kk) the *E. coli* rseA gene coding for a membrane protein with anti-sigmaE activity;
- ll) the *E. coli* rseC gene coding for a global regulator of the sigmaE factor;
- mm) the *E. coli* sucA gene coding for the decarboxylase subunit of 2-ketoglutarate dehydrogenase;
- nn) the *E. coli* sucB gene coding for the dihydrolipoyl transsuccinase E2 subunit of 2-ketoglutarate dehydrogenase;
- oo) the *E. coli* sucC gene coding for the β -subunit of succinyl-CoA synthetase;
- pp) the *E. coli* sucD gene coding for the α -subunit of succinyl-CoA synthetase;
- qq) the *E. coli* adk gene coding for adenylate kinase;
- rr) the *E. coli* hdeA gene coding for a periplasmic protein with chaperonin-type function;
- ss) the *E. coli* hdeB gene coding for a periplasmic protein with chaperonin-type function;
- tt) the *E. coli* icd gene coding for isocitrate dehydrogenase;
- uu) the *E. coli* mglB gene coding for the periplasmic, galactose-binding transport protein;
- vv) the *E. coli* lpd gene coding for dihydrolipoamide dehydrogenase;
- ww) the *E. coli* aceE gene coding for the E1 component of the pyruvate-dehydrogenase complex;
- xx) the *E. coli* aceF gene coding for the E2 component of the pyruvate-dehydrogenase complex;
- yy) the *E. coli* pepB gene coding for aminopeptidase B;
- zz) the *E. coli* aldH gene coding for aldehyde dehydrogenase,
- aaa) the *E. coli* bfr gene coding for the iron-storage homoprotein;
- bbb) the *E. coli* udp gene coding for uridine phosphorylase; and
- ccc) the *E. coli* rseB gene coding for the regulator of sigmaE-factor activity.